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☐ 1: [Q11130](#). Reports Alpha-(1,3)-fucos...[gi:1730137]

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**LOCUS** Q11130 342 aa linear PRI 04-DEC-2007  
**DEFINITION** Alpha-(1,3)-fucosyltransferase (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 7) (FucT-VII) (Selectin-ligand synthase).  
**ACCESSION** Q11130  
**VERSION** Q11130.1 GI:1730137  
**DBSOURCE** swissprot: locus FUT7\_HUMAN, accession [Q11130](#); class: standard. extra accessions: Q6DK54 created: Oct 1, 1996. sequence updated: Oct 1, 1996. annotation updated: Dec 4, 2007. xrefs: [X78031.1](#), [CAA54962.1](#), [U11282.1](#), [AAA20468.1](#), [U08112.1](#), [AAA56869.1](#), [AB012668.1](#), [BAA32819.1](#), [AL807752.10](#), [CAI12771.1](#), [BC074746.2](#), [AAH74746.2](#), [BC086312.1](#), [AAH86312.1](#), [A54057](#) xrefs (non-sequence databases): RefSeq: [NP\\_004470.1](#), UniGene: [Hs.457](#), Ensembl: [ENSG00000180549](#), GeneID: [2529](#), KEGG: [hsa:2529](#), H-InvDB: [HIX0034839](#), HGNC: [4018](#), MIM: [602030](#), PharmGKB: [PA28434](#), ArrayExpress: [Q11130](#), CleanEx: [HS\\_FUT7](#), GermOnline: [ENSG00000180549](#), GO: [0005794](#), GO: [0016021](#), GO: [0046920](#), GO: [0042355](#), GO: [0006486](#), InterPro: [IPR001503](#), PANTHER: [PTHR11929](#), Pfam: [PF00852](#)  
**KEYWORDS** Glycoprotein; Glycosyltransferase; Golgi apparatus; Membrane; Signal-anchor; Transferase; Transmembrane.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (residues 1 to 342)  
**AUTHORS** Natsuka, S., Gersten, K.M., Zenita, K., Kannagi, R. and Lowe, J.B.  
**TITLE** Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyltransferase capable of synthesizing the sialyl Lewis x determinant  
**JOURNAL** J. Biol. Chem. 269 (24), 16789-16794 (1994)  
**PUBMED** [8207002](#)  
**REMARK** NUCLEOTIDE SEQUENCE [MRNA]. Erratum: [J Biol Chem 1994 Aug 12;269(32):20806]  
**REFERENCE** 2 (residues 1 to 342)  
**AUTHORS** Natsuka, S., Gersten, K.M., Zenita, K., Kannagi, R. and Lowe, J.B.  
**TITLE** Molecular cloning of a cDNA encoding a novel human leukocyte alpha-1,3-fucosyltransferase capable of synthesizing the sialyl Lewis x determinant  
**JOURNAL** J. Biol. Chem. 269 (32), 20806 (1994)

PUBMED 8051184  
 REMARK SEQUENCE REVISION.  
 REFERENCE 3 (residues 1 to 342)  
 AUTHORS Sasaki,K., Kurata,K., Funayama,K., Nagata,M., Watanabe,E., Ohta,S., Hanai,N. and Nishi,T.  
 TITLE Expression cloning of a novel alpha 1,3-fucosyltransferase that is involved in biosynthesis of the sialyl Lewis x carbohydrate determinants in leukocytes  
 JOURNAL J. Biol. Chem. 269 (20), 14730-14737 (1994)  
 PUBMED 8182079  
 REMARK NUCLEOTIDE SEQUENCE [MRNA].  
 REFERENCE 4 (residues 1 to 342)  
 AUTHORS Hiraiwa,N., Hiraiwa,M. and Kannagi,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (??-MAR-1998)  
 REMARK NUCLEOTIDE SEQUENCE.  
 REFERENCE 5 (residues 1 to 342)  
 AUTHORS Humphray,S.J., Oliver,K., Hunt,A.R., Plumb,R.W., Loveland,J.E., Howe,K.L., Andrews,T.D., Searle,S., Hunt,S.E., Scott,C.E., Jones,M.C., Ainscough,R., Almeida,J.P., Ambrose,K.D., Ashwell,R.I., Babbage,A.K., Babbage,S., Bagguley,C.L., Bailey,J., Banerjee,R., Barker,D.J., Barlow,K.F., Bates,K., Beasley,H., Beasley,O., Bird,C.P., Bray-Allen,S., Brown,A.J., Brown,J.Y., Burford,D., Burrill,W., Burton,J., Carder,C., Carter,N.P., Chapman,J.C., Chen,Y., Clarke,G., Clark,S.Y., Clee,C.M., Clegg,S., Collier,R.E., Corby,N., Crosier,M., Cummings,A.T., Davies,J., Dhami,P., Dunn,M., Dutta,I., Dyer,L.W., Earthrowl,M.E., Faulkner,L., Fleming,C.J., Frankish,A., Frankland,J.A., French,L., Fricker,D.G., Garner,P., Garnett,J., Ghorri,J., Gilbert,J.G., Glison,C., Grafham,D.V., Gribble,S., Griffiths,C., Griffiths-Jones,S., Grocock,R., Guy,J., Hall,R.E., Hammond,S., Harley,J.L., Harrison,E.S., Hart,E.A., Heath,P.D., Henderson,C.D., Hopkins,B.L., Howard,P.J., Howden,P.J., Huckle,E., Johnson,C., Johnson,D., Joy,A.A., Kay,M., Keenan,S., Kershaw,J.K., Kimberley,A.M., King,A., Knights,A., Laird,G.K., Langford,C., Lawlor,S., Leongamornlert,D.A., Laversha,M., Lloyd,C., Lloyd,D.M., Lovell,J., Martin,S., Mashreghi-Mohammadi,M., Matthews,L., McLaren,S., McLay,K.E., McMurray,A., Milne,S., Nickerson,T., Nisbett,J., Nordsiek,G., Pearce,A.V., Peck,A.I., Porter,K.M., Pandian,R., Pelan,S., Phillimore,B., Povey,S., Ramsey,Y., Rand,V., Scharfe,M., Sehra,H.K., Shownkeen,R., Sims,S.K., Skuce,C.D., Smith,M., Steward,C.A., Swarbreck,D., Sycamore,N., Tester,J., Thorpe,A., Tracey,A., Tromans,A., Thomas,D.W., Wall,M., Wallis,J.M., West,A.P., Whitehead,S.L., Willey,D.L., Williams,S.A., Wilming,L., Wray,P.W., Young,L., Ashurst,J.L., Coulson,A., Blocker,H., Durbin,R., Sulston,J.E., Hubbard,T., Jackson,M.J., Bentley,D.R., Beck,S., Rogers,J. and Dunham,I.  
 TITLE DNA sequence and analysis of human chromosome 9  
 JOURNAL Nature 429 (6990), 369-374 (2004)  
 PUBMED 15164053  
 REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 REFERENCE 6 (residues 1 to 342)  
 AUTHORS Gerhard,D.S., Wagner,L., Feingold,E.A., Shenmen,C.M., Grouse,L.H., Schuler,G., Klein,S.L., Old,S., Rasooly,R., Good,P., Guyer,M., Peck,A.M., Derge,J.G., Lipman,D., Collins,F.S., Jang,W., Sherry,S., Feolo,M., Misquitta,L., Lee,E., Rotmistrovsky,K., Greenhut,S.F., Schaefer,C.F., Buetow,K., Bonner,T.I., Haussler,D., Kent,J., Kiekhaus,M., Furey,T., Brent,M., Prange,C., Schreiber,K., Shapiro,N., Bhat,N.K., Hopkins,R.F., Hsie,F., Driscoll,T., Soares,M.B., Casavant,T.L., Scheetz,T.E., Brownstein,M.J.,

Usdin,T.B., Toshiyuki,S., Carninci,P., Piao,Y., Dudekula,D.B.,  
 Ko,M.S., Kawakami,K., Suzuki,Y., Sugano,S., Gruber,C.E.,  
 Smith,M.R., Simmons,B., Moore,T., Waterman,R., Johnson,S.L.,  
 Ruan,Y., Wei,C.L., Mathavan,S., Gunaratne,P.H., Wu,J., Garcia,A.M.,  
 Hulyk,S.W., Fuh,E., Yuan,Y., Sneed,A., Kowis,C., Hodgson,A.,  
 Muzny,D.M., McPherson,J., Gibbs,R.A., Fahey,J., Helton,E.,  
 Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M.,  
 Madari,A., Young,A.C., Wetherby,K.D., Granite,S.J., Kwong,P.N.,  
 Brinkley,C.P., Pearson,R.L., Bouffard,G.G., Blakesly,R.W.,  
 Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J.,  
 Myers,R.M., Butterfield,Y.S., Griffith,M., Griffith,O.L.,  
 Krzywinski,M.I., Liao,N., Morin,R., Palmquist,D., Petrescu,A.S.,  
 Skalska,U., Smailus,D.E., Stott,J.M., Schnerch,A., Schein,J.E.,  
 Jones,S.J., Holt,R.A., Baross,A., Marra,M.A., Clifton,S.,  
 Makowski,K.A., Bosak,S. and Malek,J.

**CONSRTM** MGC Project Team  
**TITLE** The status, quality, and expansion of the NIH full-length cDNA  
 project: the Mammalian Gene Collection (MGC)  
**JOURNAL** Genome Res. 14 (10B), 2121-2127 (2004)  
**PUBMED** [15489334](#)  
**REMARK** NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 TISSUE=Lung, and Mammary gland  
 Erratum:[Genome Res. 2006 Jun;16(6):804. Morrin, Ryan [corrected to  
 Morin, Ryan]]

**REFERENCE** 7 (residues 1 to 342)  
**AUTHORS** de Vries,T., Yen,T.Y., Joshi,R.K., Storm,J., van Den Eijnden,D.H.,  
 Knegt,R.M., Bunschoten,H., Joziassse,D.H. and Macher,B.A.  
**TITLE** Neighboring cysteine residues in human fucosyltransferase VII are  
 engaged in disulfide bridges, forming small loop structures  
**JOURNAL** Glycobiology 11 (5), 423-432 (2001)  
**PUBMED** [11425803](#)  
**REMARK** DISULFIDE BONDS.  
**COMMENT** On Mar 15, 2005 this sequence version replaced [gi:527373](#).  
 [FUNCTION] May catalyze alpha-1,3 glycosidic linkages involved in  
 the expression of sialyl Lewis X antigens.  
 [CATALYTIC ACTIVITY] GDP-L-fucose +  
 alpha-2,3-Neu-N-acetyl-1,  
 4-beta-D-galactosyl-N-acetyl-D-glucosaminyl-R = GDP +  
 alpha-2,3-Neu-N-acetyl-1,4-beta-D-galactosyl-(alpha-1,  
 3-L-fucosyl)-N-acetyl-D-glucosaminyl-R.  
 [PATHWAY] Protein modification; protein glycosylation.  
 [SUBCELLULAR LOCATION] Golgi apparatus, Golgi stack membrane;  
 Single-pass type II membrane protein. Note=Membrane-bound form in  
 trans cisternae of Golgi.  
 [TISSUE SPECIFICITY] Leukocytic/myeloid lineage cells.  
 [SIMILARITY] Belongs to the glycosyltransferase 10 family.  
 [WEB RESOURCE] Name=GGDB; Note=GlycoGene database;  
 URL='http://ggdb.muse.aist.go.jp/GGDB/index.jsp'.

**FEATURES** Location/Qualifiers  
**source** 1..342  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
**gene** 1..342  
 /gene="FUT7"  
**Protein** 1..342  
 /gene="FUT7"  
 /product="Alpha- (1,3) -fucosyltransferase"  
 /EC\_number="2.4.1.-"  
**Region** 1..342  
 /gene="FUT7"

**Region** 1..14  
/region\_name="Mature chain"  
/experiment="experimental evidence, no additional details recorded"  
/note="Alpha- (1,3)-fucosyltransferase."  
/FTId=PRO\_0000221113."

**Region** 15..36  
/gene="FUT7"  
/region\_name="Topological domain"  
/inference="non-experimental evidence, no additional details recorded"  
/note="Cytoplasmic (Potential)."

**Region** 37..342  
/gene="FUT7"  
/region\_name="Topological domain"  
/inference="non-experimental evidence, no additional details recorded"  
/note="Signal-anchor for type II membrane protein (Potential)."

**Bond** bond(68,76)  
/gene="FUT7"  
/bond\_type="disulfide"  
/experiment="experimental evidence, no additional details recorded"

**Site** 81  
/gene="FUT7"  
/site\_type="glycosylation"  
/inference="non-experimental evidence, no additional details recorded"  
/note="N-linked (GlcNAc...) (Potential)."

**Region** 161..162  
/gene="FUT7"  
/region\_name="Conflict"  
/experiment="experimental evidence, no additional details recorded"  
/note="GP -> A (in Ref. 1; AAA56869)."

**Bond** bond(211,214)  
/gene="FUT7"  
/bond\_type="disulfide"  
/experiment="experimental evidence, no additional details recorded"

**Site** 291  
/gene="FUT7"  
/site\_type="glycosylation"  
/inference="non-experimental evidence, no additional details recorded"  
/note="N-linked (GlcNAc...) (Potential)."

**Region** 304..305  
/gene="FUT7"  
/region\_name="Conflict"  
/experiment="experimental evidence, no additional details recorded"  
/note="RL -> SV (in Ref. 1; AAA56869)."

**Bond** bond(318,321)  
/gene="FUT7"

/bond\_type="disulfide"  
/experiment="experimental evidence, no additional details  
recorded"

## ORIGIN

1 mnaghgptr rrlglgvlag vallaalwll wllgsaprgt papqptitil vwhwpftdqp  
61 pelpsdtctr ygiarchlsa nrsllasada vvfhhrelqt rrshlplaqr prgqpwwas  
121 mespshtghl shlgifnwv lsyrdsdif vpygrlephw gspplpaks rvaawvvsnf  
181 qerqlrarly rqlaphlrvd vfgrangrpl casclvptva qyrfylsfen sqhrdyitek  
241 fwrnalvagt vpvlgppra tyeafvpada fvhvddfgsa relaafitgm nesryqrffa  
301 wrdrlrvrlf tdwrrerfcai cdryphlprs qvyedlegwf qa

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